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FIGURE 138

MSPPLLKLGAVLSTMMAMISNWMSTLPSLVGLNTTRLSTPDTLTQISPKEGWQVYSSAQDPDG
RCICTVVAPEQNLCSRDAKSRQLRQLLEKVQNMSQSIEVLNLRTRQDFQYVLKMETQMKGLKA
KFRQIEDDRKTLMTKHFQELKEKMDLPLIPVLEQYKTDAKLITQFKEEIRNLSAVLGTGIE
EIGAYDYEELHQRVLSLETRLRDCMKKLTGCKLMKITGPVTVKTSGTRFGAWMTDPLASEKNN
RVWYMDSYTNNKIVREYKSIADFSGAESRTYNLPFKWAGTNHVVYNGSLYFNKYQSNIIIKY
SFDMGRVLAQRSLEYAGFHNVPYPTWGGFSDIDLMADEIGLWAVYATNQNAGNIVISQLNQDT
LEVMSKSWSTGYPKRSAGESFMICGTLYVTNSHLTGAKVYYSYSTKTSTYEYTDIPFHNQYFHI
SMLDYNARDRALYAWNNGHQVLFNVTLFHIKTEDDT

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 33-37, 95-99, 179-183, 299-303, 465-469

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 215-219

Tyrosine kinase phosphorylation site.

amino acids 106-114

N-myristoylation sites.

amino acids 9-15, 31-37, 235-241, 239-245

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FIGURE 139

GAAGCAGTGCAGAGAGGAGAGCGGAGCGGAGCTGCCGCTGAGCAAAGGCCCTTCACCAATGGCCG
AGTCCCCCGGCTGCTGCTCCGTCTGGGCCCCGCTGCCCTCCACTGCCCTGTATAGCTGCCACTGGA
GGAATGCCCCAGAGAGAGGATGCAAACAGCAAGTGCGACTGTATCTGGTTTGGCCTGCTCT
TCCTCACCTTCTCTCTTCCCTGAGCTGGCTGTACATCGGGCTCGTCTTCTCAATGACCTGC
ACAACTTCAATGAATTCCTCTTCCGCCGCTGGGGACACTGGATGGACTGGTCCCTGGCATTCC
TGCTGGTCATCTCTCTACTGGTCACATATGCATCCTTGCTATTGGTCTGGCCCTGCTCCTGC
GGCTTTGTAGACAGCCCTGCATCTGCACAGCCTCCACAAGGTGCTGCTGCTCCTCATTATGC
TGCTTGTGGCGGCTGGCCTTGTGGGACTGGACATCCAATGGCAGCAGGAGTGGCATAGCTTGC
GTGTGTCACTGCAGGCCACAGCCCCATTCTTCATATTGGAGCAGCCGCTGGAATTGCCCTCC
TGGCCTGGCCTGTGGCTGATACCTTCTACCGTATCCACCGAAGAGGTCCCAAGATTCTGCTAC
TGCTCCTATTTTTTGGAGTTGTCTGGTCATCTACTTGGCCCCCTATGCATCTCCTCACCTT
GCATCATGGAACCCAGAGACTTACCACCAAGCCTGGGCTGGTGGGACACCGAGGGGCCCCCA
TGCTGGCTCCCAGAAACACCCTGATGTCTTGGGAAGACAGCTGAATGCGGAGCTACTGTGT
TTGAGACTGATGTGATGGTCAGCTCCGATGGGGTCCCTTCTCATGCATGATGAGCACCTCA
GCAGGACCACGAATGTAGCCTCTGTATTCCCAACCGAATCACAGCCCACAGCAGTGACTTCT
CCTGGACTGAAGTGAAGAGACTCAATGCTGGATCCTGGTTCTAGAGAGGCGACCCTTCTGGG
GGGCCAAACCGCTGGCAGGCCCTGATCAGAAAGAGGCTGAGAGTCAGACGGTACCAGCATTAG
AAGAGCTATTGGAGGAAGCTGCAGCCCTCAACCTTTCCATCATGTTGCACTTGC CGCAGACCCC
CACAGAACCACACATACTATGACACTTTTGTGATCCAGACATTGGAGACTGTGCTGAATGCAA
GGGTGCCCAAGCCATGGTCTTTTGGCTACCAGATGAAGATCGGGCTAATGTCCAACGACGGG
CACCTGGAATGCGCCAGATATATGGACGTCAGGGAGGCAACAGAACGGAGAGGCCCCAGTTTC
TTAACCTCCCCATCAAGATCTGCCACTATTGGATATCAAGGCATTGCATAAGGATAATGTCT
CGGTGAACCTATTTGTAGTGAACAAGCCCTGGCTCTTCTCTGCTTTGGTGTGCAGGGGTGG
ATTGGGTACCACCAACGACTGCCAGCTGCTGCAGCAGATGCGTTACCTATCTGGCTATTA
CCCCTCAAACCTACCTAATCATATGGGTCATTACCAATTGTGTTTCCACCATGCTGCTTTTGT
GGACCTTCTCCTCCAAAGGAGATTGTGTAAGAAGAGAGGGAAACTGGCTTAGAAACAGCAG
TGCTGCTGACAAGGATCAACAATTTTCATGATGGAGTGAATGCCCTGCCCTGCTTCCCCACCCA
AGCCAGTCTACATTGCCCAAACAGCAAGGGTTGGAGAGTGGCTTAAGTGAATGCTTCAGGGG
TGGTGGGTGCAAGTGGGGGAGCTTTGCCAACAGGAGGTTTTGAACCATGAGGGCCCTCTGC
CCAGGTGATGGGCATTCCCTAAGCTGCTATGGAATCTGCTCCCTTTGGGGTTTTGACCTGAGA
TGTTTGGGAAGAGAGTGAGTAATGAGAAGTTTCTCCTCAATGAACTAGAACAGGGAAGTA
AAAGGGAGATTGCTCGGA

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FIGURE 140

MAESPGCCSVWARCLHCLYSCHWRKCPRERMQTSKDCDIWFGLLFLTFLLSLSWLYIGLVLLN
DLHNFNEFLFRRWGHWMDWSLAFLLVISLLVTYASLLVLALLLRLCRQPLHLHSLHKVLLLL
IMLLVAAGLVGLDIQWQQEWHSLRVSLQATAPFLHIGAAAGIALAWPVADTFYRIHRRGPKI
LLLLLFFGVVLVIYLAPLCISSPCIMEPRDLPPKPGLVGHRGAPMLAPENTLMSLRKTAECGA
TVFETDMVSSDGVFPFLMHDEHLSRTTNVASVFPTRIAHSSDFSWELEKRLNAGSWFLERRP
FWGAKPLAGPDQKEAESQTPALEELLEEEAAALNLSIMFDLRRPPQNHTYYDTFVIQTLETVL
NARVPQAMVFWLPDEDNANVRQRRAPGMRQIYGRQGGNRTERPQFLNLPYQDLPLLDIKALHKD
NVSVNLFVVNKPWFLSLLWCAGVDSVTTNDCQLLQQMRYPIWLITPQTYLIIWVITNCVSTML
LLWTFLLRFRFVKRGKTGLETAVLLTRINNFMM

Important features of the protein:**Transmembrane domains:**

amino acids 38-60, 83-107, 122-138, 156-173, 189-210, 484-506

N-glycosylation sites.

amino acids 349-353, 362-366, 415-419, 442-446

N-myristoylation sites.

amino acids 163-169, 413-419, 523-529

Leucine zipper pattern.

amino acids 93-115, 109-131

Glutamine amidotransferases class-II active site.

amino acids 1-13

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FIGURE 141

TGCGCGCGCCGGGCTGGGACCGAGCGCAGCAGCAGCAGCCGCGCGCGCGCGCAGAGATTGTCCTGAACCGGAGC
TGGCGGAGGAACTTTTCTTTTTCCTCTCCCTCCGCGGAGGAGGAGGAGGAGGAGCGAAGCTCCGCG
CGCGCCCGCAAGGCTCTCGGGCTCGGGGTCGGGCGCGGCCCGCAGAGGAGCGGGGGCTCGCCCGCGAGGCGAGG
CGCGCCCGCGGGGGCCCGAGAGGGGCGGCTGAGCAGCGGGCTGCTGTGTCGGCGGGCGGGGGCGGCTGTGCCCGC
CGCAGGGAGAGGGCCGCCCCCGCTCCGAGCCCGCTGCGAGAGGAGAGCGCGCGCGCGGAGAGAGCTGTAATTCT
TGTTGGCGGCGGAGCAGGSGGTTGGCCGCTCGGGGCACTCTGTGCTCTGCTGCTGGGGTGTGCTGCTGTGCTGGC
CGCTCTCGGCGACCGGGCGCTGGTCTGCTGTCCCTTGACAGACTCAAGTGTGCGAGGAGCCGAGACTGTCCGGCG
GAGCATCTGCGCAGGGGCTCTCGGGCTGCTGTACAGCTGCGCCAGCGAGGAGCAGAGACTCGGGCGCGACACTT
CGGGATTTACGGAACCTGCGACCGGGGGCTGGTGTGTATCCGCCCGCCGCTCAATGGGCATCCCTCACCC
GTACGAAGCGGGCGTTTCCGAGAACTGAGAACTGGACTGATGACCACTGCTGTTGGTTTAAACCAATGCAATGAAAA
CTTTATTGCTGGCTCAATATATCAATGGAAATGTGAATGTAAACCACTTGAACCTCGACATGCAATTCCTTTGA
TTTCCAGTCAGGATATGTGCTTTCAGCTTTAAAGAGATTTGAAGAAGAGAGCCAGATTGCTCCAGGCGCCG
CTGTGAAGTCAGGTTCTCTCAGGTTTGCTCGAAGATTCTGTTCTCGTAGGGGTTATGCTCTCTCTCGGGAGTGT
CTGCTCCCTTACCCAGCCGCTGCTGTGCAACCCGAGCGCTGTCTCGCAAGATCTCGCCAGCGGGAACACTGAA
CATACTAGTGTCAAAGAGCTCAGGGAAGCGGGGAGAGTGTGTGACCTCTATGAGTGCAAACCACTTCTTCCGGCT
GGACTCGAGGACTGTGGAATGCCCTCTGTTTTCAGACAGAGCGGCTGTCCCGGAGCTGATGAACCTCAAGTCAG
ACTACTACAGATGGTGTGCTGATTTTGCACAGAGTGGAGTGTCTCTGTGGGTTATGTGGTTTCCCGCTGTGT
TGAGTGGGATCCACTCCCGCATAGTCTCTGTGGGGATGGGACACTGGAAGTGTCTGTGATGTTCTTTGAATGT
TGTTTATGATACAAAGCCAGCTGCGTATTAACATGTGGAATATTATGATGAGACACTTGTTCGAATGGACAA
CTCTGGGTTCTGTGATGCGCAAGGGGGCTTCCATCTGCTTACTCGCCAGTGTGGTGAGATTAATCTGCAGAG
GTACTACGTCGCCGAGGAGAGTGTGCCAGTGTCTGGAAGTCCAGTGTATCTTTTATAATCCCGCTGGCTGT
TACTGCCATGGCTGATCTCTTCCCGACGAGAGCTGGTGGCGGGAAGACGACTGACATCTTGCAGCTTCCGCTCAA
CGTGAAGCCGCACTCGGTTGCGACGCTCTGCGGACGAGACTGTCAACAACTCTGTGAAGTGCCTGGGAGTGTG
CCCTGTGTGCGGAAGAACCAACCATCATCAGACTGTACCACTGCATGTGGGAGGATTACAAACTGCATCTGAC
GGGAAGAGCTGCAATTAATGGTTCAACACGATACAAATGGTTGTGCGACTGTCAGTGCGATAAACCGCAGGAG
GACTGTGTGCAAGCTTAACAAAGGCTGCACACTGTGAACCTGTCCCTCTGGTTTCCCTATGATGCCAAACTGTGA
GATCTGTGAGTGGCGCGGAGGCCGCAAGAGTGTGACCAATAATCTGTGCAAGATTTGTCCACTTGGATTGCT
GAGATATACAGCAGCGGTGTGACATCTGTGCTGTGAGAAGTGTCCAGAGCTCTCATGCTAGATCTGCCCCTTT
GGGTTTCCAGGAGCAGCTCAGCGGCTCTTATCTGTCAAAGTGCAGAGGCGCTCTGCTCAGCTGGGGCCACCAT
CTGTGTGGGCACTTGTCTCACCGTGGATGTGTATCATATAAAATGAGGAGAGCTGCGACGATGGGTGTGGGGA
ATGTGATCTCTCAATGGCGGAATGTGTGCTCCCTGTATCACTGCCCGTGCTGCTCTGTGGCAACCCCAT
TCACCTGTGCAGTGTGTCGCCCATCATGTGCGAGTCTGTGCTGTGCGAGGCGAGGCTCAGTATCTGCTCCAT
TTGCCACGCCCTCTGGAGGAGAACTTTTGTGGAGAGGAGGAGGCTGGAACATTTGACTCTACTGCTCCACTT
CCACAGCGGAGCGGGGTGCTGTGTGAGACAGAGGTGTGCCACCGCTGCTGTGCGAGAACCCCTCAGCGACCCAGG
TTCTGTGTGCCACAGGTTACAGATTCAAGCTTCTGGGCTTCTGTTCGCCGAATACAGCGTACCTGAATATCTG
CAAAATATGAGAGGATATATATCCGCTGACGTGAGCTCGTGAAGCTGACGTTTGTACCGCTGATTCGAT
TGATAGCTTAATAGCTGTTTCTGTGCTGCTGCTCTGTGATCTGTGTGTAAGACACTGTCTGTGAGAAAGGCCA
TGTTGTTGCCCTCATGATAGAGACAAATTCAAAGAGAGTGTGTGCCACTTCAGTGGGAAGCCCTATGSCCA
CGAGAGAGGCTGGGCACTTGACAGTGCACCCATCTGCTATGCTGCTCGGCCAGCCACTCTCTGCTCAGCGCTCAG
CTGCGCCCCCTCTGCCCTGTGTGAGGCCATTAAGCTGGAAGGAAGTTGCTGCCCAATGTGTGCAGAAATGTATGT
CCGAGCAACCAACCAATATACCATTGAGAGACAAACCATCGAGGAGAGGCTGACCTGGAGGTTCCCTGTGTGGCC
CAGCCCTAGTGAATATGATGTGCTATCTCCTAGAGATATGGGTCACTCCAGTGAAGTTACGAGATACAC
GCTGCACCCAAGTGAAGATTCTTCACTGGACTCCATTGCTCAGTTCTGGTTCCCATTAATATATGCTCTTAT
TATATAGACTTCTATTCATCAATCAGAGAACAGTGGATCCACTGCTTGTGTTGATCGAACCCCTACTTA
GGCTTTCTTTCAATAAATTCAGCTAGTATCTGTGCACTGCAAGAAAGGACAGAGTTCAGGTTGGAAGATTCCA
GAGATCTGTGAAGATTGCGAGACCAAGATGCAAGTACTGCTGGTTCTACAGATCGAAACAGCAACACTACA
GGCAGACATATTTACCAACAGCTTGAAGAAAGGCACTAGATGAGTGTTCAAAGACGGGAGACGACTAAAT
CTGCTCTAAAAGCTAAACTAGAAATTTGTGCATCTGCTTATGTGAGTGTGATTTGGATTGTGACTGTGATGTACAGCC
TAGBCCTTTACTGGGATGGCTCTGTGCTACAGCAATGTGTGAGACAGAGATTCACCTTTTCTCAAAAAA

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FIGURE 142

MYLVAGDRGLAGCGHLLVSLGLLLLLLARSCTRALVCLPCDESKCEPRNCPGSIQGVCGCC
 YTCASQRNESCGGTFGIYGCDRGLRCVIRPPLNGDSLTEYEAGVCEDENWTDQLLGFKPCN
 ENLAGCNININKCECENTIRTCSPFEFPSSQDMCLSAKRIEKEPDCSKARCEVQFSRCPPE
 DSVLIEGYAPPGECCPLPSRCVCFNPFAGCLRKVCQPGNLLNVLKSKASGKPGCECDLYECKPVFG
 VDCRTVECPVPVQQTACPPDSYETQVRLTADGCCTLPTRCECLSGLCGFVCEVGSTPRIVSRG
 DGTGPKCCDVFECVNDTKPACVFNNVEYYDGDMMFRMDNCRFCRCQGGVAICFTAQCGEINCE
 YYVPEGECCPVCEDPVYFPNNPAGCYANGLILAHGDRWRDDCTFCQCVCNGERHCVAIVCGQT
 CTNFPVKVPEGCCPVCEPTIITVDPPACGELSNTLTGKDCINGFKRDHNGCRCTQCINTEEL
 CSERKQGGCTLNCFFGLTDAQNCEICECRPRPKKCRPIICDKYCPGLGLLNKHKGCDICRCKK
 PELSCSKICPLGFQQDSHGCLICKREASASAGFPILSGTCLTVDGHHHKNESWHDGCRECY
 CLNGREMCALITCPVACGNPTIHPGQCCPSCADDFVQKPELSTPSICHAPGGGEYFVEGETW
 NIDCTQCTCHSGRVLCETEVCPPLLCQNPSTQDSCCPQCTDQPFRLSRNNSVFNKYCKND
 EGDIFLAESWKPVDCTSCICIDSVISCFSESCPSVSCERPVLRKGCCCPYCIEDTIPKKVVC
 HFSGKAYADEERWDLDSCTHCYCLQGQTLCTSVSCPLPCVEFINVEGSCCPMCFEMYVPEPT
 NPIIEKTNHRGVEVDLEVPFWPTPSENDIVHLPRDMGHLQVDYRDNRLHPSEDSSLDIASVVV
 PIICLSLIIAFLFINQKKQWIPLLCWYRTPTKPSINNQLVSVDCCKGTRVQVDSSQRLMRI
 AEPDARFSGFYSMQKQNHQLQADNFYQTV

Important features of the protein:**Signal peptide:**

amino acids 1-34

Transmembrane domain:

amino acids 940-962

N-glycosylation sites.

amino acids 71-75, 113-117, 330-334, 474-478, 746-750

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 992-996

N-myristoylation site.

amino acids 9-15, 58-64, 61-67, 75-81, 79-85, 362-368, 402-408, 407-413,
 439-445, 492-498, 511-517, 551-557, 558-564, 586-592, 606-612, 625-631,
 845-851

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 52-63, 844-855

Cell attachment sequence.

amino acids 314-317

Leucine zipper pattern.

amino acids 3-25

Eukaryotic thiol (cysteine) proteases cysteine active site.

amino acids 57-69

VWFC domain proteins.

amino acids 448-456, 382-390

C-terminal cystine knot proteins

amino acids 60-86

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FIGURE 144

MVARVGLLLRALQLLLWGHLDQAERGQELRKEAEAFLEKYGYLNEQVPKAPTSTRFSDAI
RAFQWVSQLPVSGVLD RATLRQMTRPRCGVTD TNSYA AWAERISDLFARHRTKMRRKKRFAKQ
GNKWKYQHLSYRLVNWPEHLPEP AVRGAVRAAFQLWSNVSALEFWEAPATGPADIRLTFFQGD
HNDGLGNAFDGPGGALAHAF LPRRGEAHFDQDERWSLSRRRGRNLFVVLAEIGHTLGLTHSP
APRALMAPYYKRLGRDALLSWDDVLAVQS LYGKPLGGSVAVQLPGKLF TDFETWDSYSPQGRR
PETQGPKYCHSSFDAITVD RQQQLYIFKGSHEVEAADGNVSEPRPLQERWVGLP PPNIEAAAV
SLNDGDFYFFKGGRCWRFRGPKPVWGLPQLCRAGGLPRHPDAALFFPPLRRLILFKGARYYVL
ARGGLQVEFYPRSLQDWGGIPEEVSGALPRPDGSIIFFRDDR YWRLDQAKLQATTSGRWATE
LPWMGCWHANS GSALF

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 164-168, 355-359

N-myristoylation sites.amino acids 92-98, 153-159, 193-199, 202-208, 288-294, 368-374,
509-515**Amidation site.**

amino acids 312-316

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 237-247

Matrixins cysteine switch

amino acids 231-262, 271-284

Hemopexin domain protein

amino acids 66-108, 231-262

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FIGURE 145

GCCGGCTAGGGCGCCGAGCCGACGCGAGCCGGGGCTCCGAGAGGCGCGCACTGGGGCTGGGACTGCGCGGGC
 CCGCGCTGCGAGCGCCACTGAGCGGTCGCGCAACTTCGAGGGCACAGCGCGGAGCCAGCGCGCTGAGAGAC
 CCGGAGGCCAGGAGGGCGCGCCGGAGGCTCGTTCGAGAGCCGGCGCCAGCCACCGCGCTCTCGAGTGCCGAG
 CGGCCCTCCGCGACAGCTGGCTTCGCTGCCCCACGGAAGGCAGGGGCTGGCGCTGCCGGCGCGCGGGAGGAC
 GCGAGGAGGCGCGCGCGCGCGGAGACGGCGCGGAGACTGGGGCGAGGAGACAGCCCTGGGGGAGAGGCG
 GCGCGAACCGAGCCCGCGGAGCAGTGGGCGCGGAGCGGAGCTCGGGCGCGCTGCTGCTGGCACTGCTGCTCT
 CTGGGACCCGAGGCTGAGCAAGCAGGCACTGATTCTGGCAGCGAGGTGCTCCCTGACTCCTTCCCGCTCAGCGCC
 AGCAGAGCGCTGCCCTACTTCTCGAGGAGCCACAGGACGCTACATTGTGAAGAACCAAGCTCTGGAGCTCCG
 CTGCCGCGCCTTCCCGCCACACAGATCTACTTCAAGTGCAACGGCGAGTGGGTGAGCGAGAACGACCAGCTAC
 ACAGGAAGGCTGGATGAGGCCACCGGCTGCGGGTGGCGAGGTGCAGATCGAGGTGTCCGGCGAGCAGGTGGA
 GAGGCTCTTTGGGCTGGAGGATTACTGGTGCCAGTGCGTGCCCTGGAGCTCCGCAAGGCACCACCAAGAGTCGCGC
 AGCTACGCTCCGATCGCTACTCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCTGGACCA
 TGAGGTCTCTCTGAGTGCCGCCGCCGCGGAGGGGGTGCTGTGGCGAGGTGGAAATGGCTCAAGAATGAGGATGT
 CATCGACCCCAACCGAGGACCAACTTCTGCTCACTATCGACCACAACCTCATCATCCGCGAGCGCCGCTGTCT
 GGACACTGCCAACTATACCTGCGTGCCCAAGAACATCTGTGCCAAACCGCGGAGACCACTGCCACCGCTCATCTGT
 CTACGTGAATGGCGGCTGCTCGAGCTGGCGAGTGGTCAACCTGCTCCAAACGCTGTGGCGCGAGGCTGGCAAGAA
 GCGCACCCGAGCTGCACCAACCCCGCTCCACTACACGGAGGGGCTTCTGCGAGGGCCAGGCACTCCAGAAAGC
 CGCTTGCACCACTATCTGCCAGTCGATGGGGCTGGAGCGAGTGGAGCAAGTGGTCAAGCTCCGCGAGCACTGAGTG
 TGGCCACTGGCGTAGCGCGAGTGCTAGCGGCCCAACCCAGAGACGGAGCCGTGACTCGACGCGAGCGCTGTCT
 CGACTCTAAGAACTGCACAGATGGGCTGTGCATGCAAAATAAGAAACTCTAAGTGAGCCCAACAGCAGCACTGTCT
 GGAGGCTCTCAGGGGATCGAGGCGGCTGTATGCGGGGCTCTGTGGTGCCATCTTCGGGCTCGTGGCAATCTCTATGGC
 GGTGGGGTGTGCTGTACCGCGCACTGCCGTGACTTCGACACAGACATCACTGACTCATCTGCTGCCCTGAC
 TGGTGGTTTGCACCCGCTGACCTTAAAGACGCGCAAGGCCAGCAACCCGAGCTCTCACTACCCCTCTGTGCCCTC
 TGACCTGACAGCCAGCGCGGCTATACCGCGGACCCGTGTATGCCCTGCAGGACTCCACCGCAAAATCCCCAT
 GACCAACTCTCTCTGCTGCGACCTTACCAAGCTTAAAGTCAAGGTCTACAGCTCAGCAGCAACCGGCTCTGG
 GCCAGGCTGCGAGATGGGGCTGACTGCTGGGGGCTTCTGCCGCTGGCACATACCTTAGCGATTTCGCCCGGGA
 CACCACTTCTGCACCTGCGCAGCGCCAGCTCCGTTCCAGCAGCTCTTGGCGCTGGCAGACCCAGCGAG
 CAGCGTCAGCGGCACTTTGGCTGCTGGTGGGAGGCTCAGCATCCCGGCGACAGGGGTGAGTCTGCTGGTGCC
 CAATGGAGCCATTTCCCGAGGGCAAGTTCTACGAGATGTATCTACTCATCAAGAGGCAAGAAATACCTCCCGCT
 TTCAGAAGGACCCAGCAAGTATTGAGCCCTCGTGACCTGTGGACCCACAGGCTCCTGTGTGCCGCCCGCT
 CATCTCACTACCTGCCCACTGTGCCGAAGTCAGTGCCCGTGACTGGATCTTTCACTCAAGACCCAGGCCACCA
 GGGCCACTGGAGGAGGTGGTGACCTGGATGAGGAGACCTGAACACACCTGCTACTGCCAGCTGGAGCCAG
 GGCTGTGCATCTCTGCTGGACAGCTGGGCACCTAGCTGTTACCGGGCGAGTCTATTTCCCGCTCAGCAGTCAA
 GCGGCTCCAGCTGGCGGTCTTCGCGCCCGCCCTCTGCACCTCCCTGGAGTACAGGCTCCGGGTCTACTGCTGGA
 GAGACCGCTCTAGCACTGAAGGAGGTGCTGGAGCTGGAGCGGACTCTGGCGGATACTTGGTGGAGGAGCCGAA
 ACCGCTATTGTTCAAGGACGTTACCAACACTCGGCTCTCCCTCCATGACTCCCCCATGCTCCCTCTTGGAGGAG
 CAAGCTGCTGGCCAAATACCAGGAGATCCCTTCTATCAGATTGGAGTGGCAGCAGAGGCCCTTCCACTGCAC
 TTTCCACTGGAGAGGCACAGCTTGGCTCCACAGAGCTACCTGCAAGATCTGCGTGGCGCAAGTGGAGGGGA
 GCGCCAGATATTTCAGCTGCATACCACTCTGGCAGAGACCTGTGGCTCCCTGGACACTCTCTGCTCTGCCCC
 TGGCAGCACTGATCACCACCCAGCTGGGACCTTATGCTTCAAGATCCCAGTGTCCATCCGCGAAGATATTGCA
 CAGCTCAGTCAGTCCCACTACCGGGCAATGACTGGCGGATTTAGCACAGAGCTCTCTATGGACCGGTATGCA
 GAATTACTTTGCCACCAAGCGAGGCCACCGGGTGTGATCTGGACCTCTGGGAAGCTCTTGCAGCAGGACGATGG
 GAACTCAACAGCTGGCGAGTCCCTTGGAGGAGATGGGCAAGAGTGAGATCTGTGGGCTGTGGCCACCGAGCG
 GGAATGCTGAAGCTCTTGGGACAGCGGGCTGGCAGGGACTGCGAGGAGGCAAGGTGAGGAGGCTTGGGAGCGCC
 TCTGATGGGAGTGTCTTGGCTCTGCTGCTCCAGTTACAGCGAGAGTGGCTCTCCCTCGCTCTCTCCCA
 CCCCAGACCATGACCAAGCTTAGAAAAATCCATGTACTCTGTTTAGAGGGCCACAGATTTCTCTCCACCCGCT
 GCTCTCTCTCTCTTGGCTGAGATCTCTGTGCGAGGAACCAAGATGGGCTGAAGCTCTGGAGGCACTTGGTGG
 GCGCGGCGAGCGAGGCGGCTCCCTCCACCCCGCCCTCAGCCCGGCAACTCTCTGGTTCGGTGGGTTTTAG
 TTCGGCTCTCTGCTTTCTCTCTCGGTATTGATTCTCTCTTCTCCCTAAGCGCCCTTCTGCTTCCAGCGCTTT
 TCTCTTTGAAGAGTCAAGTACAACTCAGACAAATGCTTTCTCTGTCGCAAGGAAAAAGGCAAGGAAAAAGAA
 AGAAGGCTTCAGACCGCTAGTAGGCTCAAGAGAAAGAAAAACCAACCAAGGCGAAAGAAAAACCGAG
 TTTCTTAGGAAACGCAAGCAATTTATTATACAGATATTGGGATAAGTCTTTTAAAA

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FIGURE 146

MGARSGARGALLALLLCWDPRLSQAGTDSGSEVLDPDSFPSAPAEPLPYFLQEPQDAYIVKKN
 PVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLEDEATGLRVREVQIEVSRQQVEELFGLDY
 WCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPGKEVPLDHEVLLQCRPPEGVPVAEVEWLK
 NEDVIDPTQDTNFLTIDHNLIIQARLSDTANYTCVAKNIVAKRRSTATVIVYVNGGWSSW
 AEWSPCSNRCGRGWQKRTCTNPAPLNGGAFCEGQAFQKTACTIONCPVDGAWEWSKWSACS
 TECAHWSRSECMAPPONGGRDCSGTLLDSKNCTDGLCMQNKLTSDPNSHLLEASGDAALYA
 GLVVAIFVVAAILMAVGVVVYRRNCRDFTDITDSSAALTGGFHPVNFKTARPSNPQLLHPSV
 PPDLTASAGIYRGVYALQDSTDKIPMTNSPLLDPLPSLKVVKVYSSSTTSGSGPLADGADLLG
 VLPPTGYPSDFARDTHFLHLSASLGSQQLLGLPRDPGSSVSGTFGCLGGRLSIPGTGVSLV
 PNGAIPQGFYEMYLLINKAESTLPLSEGTQTVLSPSVTCGPTGLLLCRFVILTMPHCAEVSA
 RDWIFQLKTAQAGHWEVVTLEETLNTPCYQLEPRACHILLDQLGTYYVFTGESYSRSVAVK
 RLQLAVFAPALCTSLEYSRLVYCLEDTFVALKEVLELERTLGGYVVEPKPLMFKDSYHNLR
 SLHDLPHAHWSKLLAKYQEIFYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEG
 QIFQLHTLAETPAGSLDLCAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDRM
 LAQKLSMDRYLNYFATKASPTGVILDLWEALQDDGLNSLASALEMKGKSEMLVAVATDGC

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 374-395

N-glycosylation sites.

amino acids 222-225, 347-350

Glycosaminoglycan attachment site.

amino acids 492-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 233-236, 234-237

Casein kinase II phosphorylation sites.

amino acids 30-33, 87-90, 251-254, 341-344, 359-362, 629-632, 651-654, 706-709, 757-760, 827-830, 925-928, 941-944

Tyrosine kinase phosphorylation sites.

amino acids 216-223, 773-780

N-myristoylation sites.

amino acids 2-7, 6-11, 27-32, 96-101, 137-142, 179-184, 247-252, 281-286, 334-339, 379-384, 491-496, 495-500, 509-514, 542-547, 547-552, 550-555, 553-558, 560-565, 611-616, 785-790, 834-839, 844-849

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 541-551

ATP/GTP-binding site motif A (P-loop).

amino acids 926-933

Growth factor and cytokines receptors family signature 2.

amino acids 306-312

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FIGURE 147

GAGAGGGACAGAGGCTGGAGAAGGATGTATGECCTGCCTGGGCTTGTCTGTTCCTCTCTGAGCCTGAGCCCTT
 ACCTTCCTGACCCCAAGAGCACACACTGGCTCTGCTGGCTCCCTGCTGGGCGCTGGGCGCTGGGCGCTGGGCGCTGA
 GTCACTGGCTGACGGGGCCGACACTGCAAGTTCTTGGCCGGCAGAGCACCTGGACATTCCACCCAGCAGCA
 GGGCCCGGTGGCTGGCCCTCGAGTTGGTGGCCAGGAGCTCCTGGACTCCCTCTATGGCACCTGCGCCGCTTCC
 TCTCGGTGGTGCAGCTCAATCTTTCCCTTCAGAGTTGGTAAAGGCCCTACGAATGAGCTGGCCTCGGTGAAG
 TGAATGAGGTGTGCGGTACGAGGGCGGCTACGTGGTATGCGCTGTGATCGCGGCCCTCTACTGCTGCTGGTGC
 CCACTGCGGGCTTTGCTTCTGCTGCTGCGCTGCCACCGGCGCTGCGGGGGACGAGTGAAGACAGAGCAAGG
 CGCTGGCCTGTGAGCGCGCGCGCCCTCATGGTCTTCTGCTGCTGACCACTCTTGTGCTGATTGGTGGTCT
 GTGCTTTGTGACCAACACGCGCAGCATGAACAGATGGGCCCCAGCATCGAGGGCCATGCTGAGACCTGCTCA
 GCTCTGGGGCTGTGCTCTGATGTCCCCAAGAGCTGCAGGCCGTGGCACAGCAATTCCTCGCTGCCCGAGGAGC
 AAGTCTCAGAGGAGCTGGATGGTGTGGTGTGAGCAATTGGGAGCGGATCCACACTCAGCTCAGGAGCTCCGTGT
 ACCCTTGTGTGGCGCCCTGGGCGAGTTTGGGCCAGTCTCTGCAAGTCTCCGTGCACCACTGCAAACTTGAATG
 CTACAGTGGTAGAGCTGCAGGGCGGGCAGCAGGAGCTGGAGCCAGCCATCCGGGAACACCGGGACCGCTCCTTG
 AGCTGCTGCAGGAGGCCAGGTGCCAGGAGATTGTGAGGGGCCCTTGAGCTGGGCGGCCACCTTGAGAGCTGGGTG
 CTGACTTCAGCCAGGTGCCCTCTGTGACCACTCTCTGCACAGCTAAAGAGTGTCCCCGAGGGCACTTCTTCCA
 GCATGGTCCGAGGAGAGACAGCACTTCAACGCCCTTCCAGCCTGGCTGCCATGCACACATCCAGGCTGGTGC
 AAGAGCTGAAGAAGGCAGTGGCCAGCAGCGGAGGGGTGAGGACACTGGCTGAAGGGTTCCCGGCTTGCAGG
 CAGCTTCCCGCTGGGCGCCAGGCATCGAGGAGGTGGAGGAGAGCAGCCCGCTACTCTGAGGAGGTGCAGAGT
 ACGAGACTACAGGTGGATGCTGTGGGCTGGCTGCTGTGCTGCTGCTTATTCCTGTGGTGTCTGCAACTCTGGG
 CGCTCAATCTGGGCTCTGGGGCTGTCTGCCAGGAGCAGCCCGCCAGCCACCGAGGCAAGGGCGAGGCTGGAG
 CCGCTCTTCTCATGGAGGTGTGGGCTCAGCTTCTTCTTGTGCAACCTCATCTCTCTGGTGTGGCAGCT
 TCTCGTGGTGGCAACGTGCAGACGTGTGTGTGCGGAGCTGGGAGAACGGCGAGCTCTTTGAGTTTGCAGACA
 CCGCAGGAGGACTGCCCGCTCCATGAACCTGTGCCAATCTTGGCCTGAGGAGAAGACATCAGCATCCACCAAG
 CTTATCAGCATGCAGGAGGGGGCAGCGCTCTGGACAGTCTCTCAGCTCAACGACTCTTACGACCTGGAGGAGC
 AACTGGATATCAACAGTATACCAACAGCTACGGCAGGAGTTGCAGAGCTTGAAGTAGACACACAGCTGGG
 ACCTGCTGAGCTCAGCCGCCCGCGGAGCTGGAGGCCCTGCAGAGCAGTGGGCTTCAGGCGATCCACTACCCCG
 ACTTCTCTGTTAGATCCAGAGGGCGCTGGTGAAGACAGCATGGAGCAGCTGGCCCGAGGAGCTGCAAGGACTGG
 CCCAGGCCAAGACAACTTCTGTGCTGGGGCAGCGGCTGCAGGAGGAGGCCCAAGGACTCAGAAACCTTACACAGG
 AGAAGGTGCTCCCCAGCAGAGGCTTGTGGCAAGCTCAACCTCAGCGTCAGGGCGCTGGAGTCTCTTGCCCGGA
 ATCTCCAGCTGGAGACTCAGATGTCTAGCCAAATGTCACCTACCTGAAAGGAGAGCTGCTTCTGCTGGGAGCCA
 GGATCCTGAGGAATGTGAGTGAAGTGTCTTCTGGCCCGGGAGATGGGCTACTTCTCCAGTACGTGGCTGGGTGA
 GAGAGGAGGTGACTCAGCGCATTGCCACCTGCGAGCCCTCTCCGGAGCCCTGGACACAGAGCGTGTGATCTGT
 GTGACATGATGGCTGACCCCTGGAATGCCCTTCTGTTCTGCTGGCATGGTGCACCTTCTTCTGATCCCGAGCA
 TCACTTTTGGCGTCAAGACCTCCAAATACTTCCGTCCTATCCGGAACGCTCAGCTCCACAGCTCTGAGGAGA
 CTCAGCTCTTCCACATCCCCCGGGTTACTCCCTGAAGCTCTAGGGCTTGTGGGGTGAGGTGACCTTGAGGCTG
 CCTGCTCCCTCTTTGATTAGCTTGGGCCACAGSACTTCCGTAGCTCTTGGCCAGAGCCAGGCTGGCATCCA
 GGCCTGGACTGTGCCAGTTTCCGGCTTACCTGGCCGCCACCTTGCCTGCTCCTTTCCACCCCTTCTGCTCAGGAC
 CCCCATTATCAGCGTCAGAATCAGATGGGACTTCTGTGACAGTGCAGAGCCAGGAGCTCCCTACAGGTTCTCACC
 CGTTACCCCATGCTGGTGGCATCTCAGAGGAAGGCTGTTCTCCACTCTGCGTGGAGCTGGAGCCCTGGGGTGG
 GACAGAGGCTCTGTCACAAACCCATCCCTTCCCGTGTGCTTCCCTTCCACCGCTCCCTCTGCCAAGCTCCG
 CCTGCCCTCTCTGAGCGCCTTGCGCCCCACACCGTCTCATCTGGCTCCACCTTGGCCGCCACTTCCCTTCT
 GTGCCCTTCTGGCCCTTGTCTTCTCCCTTAGTCCCTCTTCAACATATCTCCAGTGTGATACCTTGTGGGCCCA
 GAGACACCCCTGCCCAACCAACCACTCAGGTAAAGCCACTAATCAGGAGGGGCCACCATGGCCTAGGTGTGGG
 CTGGCTGAGGCTGCTGCTCATGGCTCTGAGCCCTTCCACTGCCCGAGGGCTTGGGCCCTCTGCGAGATCTCATC
 CAGAGTTATCTTGTGTCAGTGGGTGAGGAGGCTGTCTGAAGGCCAGGAGCTCCCTGCTGCACCACTAGTAG
 AARTGGGGGTACAGCACTTAGCTTCTCTCTGAGTGTGGCTCCCAAGGAAGGAGCTGGGAGCTGGGCGAGCTG
 GGGGCTTCCCTTACCTCTCAGAAAGGAGCATCTTCCACAGCGCCCAACCACTTCTTAGGATGATCTGTGT
 GGCCAGAACAGATTTTGACAGGCCCTTTTATCTGCGCATTTGGCCTTAGGTTATCCCGGACCTTCCCTGTG
 TCAGCCCTGAGTGTGGACACTGCGTTCAGAAATGAGGAAGAGGAGAGAGATGGACAGCTCAGATCC
 ATTAAGTGTCTCACTTCAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

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FIGURE 148

MKHTLALLAPLLGLGLGLALSQLAAGATDCKFLGPAEHLTFTPAARARWLAPRVRAPGLL
 DSYLGTVRRFLSVVQNLNPFPSSELVKALLNELASVKVNEVVRYEAGYVVCAVIAGLYLLLV
 PTAGLCFCCCRCHRRCGGRVKTEHKALACERAAALMVFLLLTLLLLIGVVCAFTVNORTH
 EQMGPSIEAMPETLLSLWGLVSDVPQELQAVAQQFSLPQEQVSELDGVGVSIGSAIHTQ
 LRSSVYPLLAAVGSLGQVLQVSVHHLQTLNATVVVELQAGQODLEPAIREHRDRLLLELQE
 ARCCGDCAGALSWARTLELGADFSQVPSVDHVLHQLKGVP EANFSSMVQEENSTFNALPA
 LAAMQTSSVVQELKKAVAQQPEGVRTLAEGFPGLEAASRWAAQALQEVEESSRPYLQEVQR
 YETYRWIVGCVLCSVVLFFVVLNLLGLNLGIWGLSARDDPSHPEAKGEAGARTLMAGVGL
 SFLFAAPLILLVFATFLVGGNVQTLVCRSWENGELFEFADTPGNLPPSMNLSQLGLRKNN
 ISIHQAYQQCKEGAALWTVLQLNDSYDLEELDINQYTNKLRQELQSLKVDTSGLDLLSS
 AARDLEALQSSGLQRIHYPDFLVQIQRPVVKTSMEQLAQELQGLAQADNSVLGQRLQE
 EAQGLRNLHQEKVVPQQSLVAKLNLVSRALESSAPNLQLETSVDLVANVTYLGELPAWAA
 RILRNVSECFLAREMGYFSQYVAWVREEVTQRIATCQPLSGALDNSRVILCDMMADFNWA
 FWFCLAWCTFFLIPSIIFAVKTSKYFRPIRKRLSSSTSSEETQLFHIPRVTSLKL

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 105-125, 153-173, 428-449, 476-500, 778-797

N-glycosylation sites:

amino acids 270-273, 343-347, 352-356, 530-534, 540-546, 563-567,
 684-688, 707-711, 725-729

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 811-815

Tyrosine kinase phosphorylation site.

amino acids 95-103

N-myristoylation sites.

amino acids 13-19, 15-21, 17-23, 26-32, 58-64, 124-130, 168-174,
 228-234, 230-236, 320-326, 338-344, 393-399, 429-435, 446-452,
 477-483, 500-506, 536-542, 644-650, 761-767

Phospholipase A2 histidine active site.

amino acids 129-137

4Fe-4S ferredoxins, iron-sulfur binding region signature.

amino acids 126-138

Mitochondrial energy transfer proteins signature.

amino acids 80-89

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FIGURE 149

CACAGCTCCCTTCCCAGGACGTGAAAAATCTGCCTTCTCACCATGAGGCTTCTAGTCCTTTCCA
GCCTGCTCTGTATCCTGCTTCTCTGCTTCTCCATCTTCTCCACAGAAGGGAAGAGGCGTCCTG
CCAAGGCCTGGTCAGGCAGGAGAACCAGGCTCTGCTGCCACCGAGTCCCTAGCCCCAACTCAA
CAAACCTGAAAGGACATCATGTGAGGCTCTGTAAACCATGCAAGCTTGAGCCAGAGCCCCGCC
TTTGGGTGGTGCTGGGGCACTCCACAGGTGTAGCACTCCCAAAGCAAGACTCCAGACAGCG
GAGAACCTCATGCCTGGCACCTGAGGTACCCAGCAGCCTCCTGTCTCCCTTTTCAGCCTTCAC
AGCAGTGAGCTGCAATGTTGGAGGGCTTCATCTCGGGCTGCAAGGACCCTGGGAAAGTTCCAG
AACTCCACGTCCTTGTCTCAATTGTCCATCAACTTTCAGAGCTATCATGAGCCAACTCACC
CCACAGGGCCTCAGTCGCCACCATGTGGGCCTCTCCAGTGCAAACCACCGAGCATTCACCAT
GACCGGTCACAGCTACAAATCCAGAGACCATCAATCCTGCTAGAGTGCAAGGTGGCAAGCACC
CAAGGGTGGCTGACCAAGACTGCAGAGTCTCCTCCATCTTCAGGTCCATTACGCCTCCTGGCA
TTTAACTACCAGCATCCAGTGGTCCCCAAGGAATCCCTTCTAGCCTCCTGACATGAGTCTGC
TGGAAGAGCATCCAAACAAACAAGTAATAAATAAATAAATAAACTCA

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FIGURE 150

MRLLVLSLLCILLLCFSIFSTEGKRRPAKAWSGRRTRLCCHRVSPNSTNLKGHHVRLCKPC
KLEPEPRLWVVP GALPQV

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 48-52

Amidation sites.

amino acids 23-27, 33-37

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FIGURE 151

CACCGGAGGGCAGCGAGCTGACGGAGCTGCGCTGCGTTTCGCTCGTTTCGCTCGCGCCCTCCA
CTGGAGCTGTTTCGCGCTCCCGGCTCCCACCGCAGCCACCCGGCAGAGGAGTGCCTACCAGC
GCCAGTGCCTCTGTGAGTCCGCAAACTCCTTGCCGCGCCCGCCCGGGCTGGGCACCAAATAC
CAGGCTACCA**ATGGT**CTACAAGACTCTCTTCGCTCTTTGTCATCTTAAGTGCAGGATGGAGGGTA
CAGAGTCTGCCTACATCAGCTCCTTTGTCTGTTTCTCTTCCGACAAACATTGTACCACCGACC
ACCATCTGGACTAGCTCTCCACAAACACTGATGCAGACACTGCCTCCCCATCCAACGGGCACT
CACAAACACTCGGTGCTCCAGTTACAGCATCAGCCCCAACATCTCTGCTTCCTAAGAACATT
TCCATAGAGTCCAGAGAAGAGGAGATCACCAGCCAGGTTTCAATTGGGAAGGCACAAACACA
GACCCCTCACCTTCTGGGTTCTCGTCAACAAGCGGTGGAGTCCACTTAACAACCACGTTGGAG
GAACACAGCTCGGGCACTCCTGAAGCAGGCGTGGCAGCTACACTGTCGAGTCCGCTGCTGAG
CCTCCACACTCATCTCCCCTCAAGCTCCAGCCTCATCACCTCATCCCTATCAACCTCACCA
CCTGAGGTCTTTTCTGCCTCCGTTACTACCAACCATAGCTCCACTGTGACCAGCACCCCAACCC
ACTGGAGCTCCAAGTGCACAGAGTCCCGACAGAGGAGTCCAGCTCTGACCACACACCCACT
TCACATGCCACAGCTGAGCCAGTGCCTCCAGGAGAAAACACCCCCAACAACTGTGTGAGGCAAA
GTGATGTGTGAGCTCATAGACATGGAGACCACCAACACCTTTCCAGGGTGATCATGCAGGAA
GTAGAACATGCATTAAGTTTCAGGCAGCATCGCGGCCATTACCGTGACAGTCATTGCGCTGGTG
CTGCTGGTGTGGAGTTGCAGCCTACCTAAAAATCAGGCATCTCTCTATGGAAGACTTTTG
GACGACCATGACTACGGGTCTGGGGAAACTACAACAACCCCTCTGTACGATGACTCCT**TAACA**A
TGGAATATGGCTGGGATGAGGATTAAGTGTCTTTATTTATAAGTGCTTATCCAGTAGAATT
AATAAGTACCTGATGCGCATGAACGACAATCTTAAGCCCTGTTTTGTGGTATGGTGTGTTTT
TGTTTTCTCTCCTCTCCTCTGGCTGCTACAACCTTCCCTTTCTGGTACAAGAAGAACATTCT
TTAAAGGTGAGTGGAGGCTGATTTGCAGCTGAAGTGGGCCAGCCTTGACCCAGCCAGGCCAGA
CCACCATGGTGAAGGTTCTTTCCCACTGCAGGACCCACTTTGAGAAGGATCGAGGAGGAGG
ATTTGGGTTGTTTTGTTAGGGGTTACTTTCAGGGGAACATTTCAATTTGTGTTATTTCTTAAC
TTCTATTTAGGAAATTACATTAAGTATTAATGAGGGGAAAGGAAATGAGCTCTACGAGGATTT
CACCTTGATGGAGAGAGCAGGGTTTTCTCAGATTCCCTTTTAATCTCTATTTATCTGGTTG
TTTCTGACAGGATGCTGCCTGCTTGGCTCTACGAGCTGGAAGCAGCTTCTTAGCTGCCTAAT
TAATGAAGATGAAATAGGAAGTGCCCTGGAGGGGGCCAGCAGGTACGCGGGCAGAATCTCT
CAGGTTGCTGTGGGATCTCAGTGTGCCCTACCTGTTCTCCCTCCAGGCCACCTGTCTCTGT
AAAGGATGCTGCTCTGTTCAAAAGGCAGCTGGGATCCCAGCCCAAGTGATCAGCAGGTT
GCATTTCAAGAAAAAGGCTATGAGATGAGCTGAGTTATAGAGAGAAAGGGAGAGGCGATGA
CGGTGTGGGGAAGTGAAGAGAAGCTGGCGGGGAGAAGGAGGCTAACCTGCACCTGAGTACTT
CATTAGGACAAGTGAGAATCAGCTATTGATAATGGCCAGAGATATCCACAGCTTGGAGGAGCC
CAGAGACTGTTTGCTTTATACCACACAGCAACTGCTGCTACTGCTTTACTGTCTGTTGGATAA
TGGCTGTAAATGTTTAAAAAC

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FIGURE 152

MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSSPQNTDADTASPSNGTHNN
SVLPVTASAPTSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVHLTTTLEEHS
SGTPEAGVAATLSQSAAEPTLISFPQAPASSPSSLSTSPPEVFSASVTNHSSTVTSTQPTGA
PTAPESPTTESSSDHTPTSHATAEPVPQEKTPPTTVSGKVMCELIDMETTTTTFPRVIMQEVEH
ALSSGSIAAITVTIVIAVLLVFGVAAYLKIRHSSYGRLLDDHDYGSWGNYNPLYDDDS

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 258-278

N-glycosylation sites.

amino acids 58-61, 62-65, 80-83, 176-179

Casein kinase II phosphorylation sites.amino acids 49-52, 85-88, 95-98, 100-103, 120-123, 121-124, 141-
144, 164-167, 191-194, 195-198, 200-203**Tyrosine kinase phosphorylation site.**

amino acids 289-296

N-myristoylation sites.

amino acids 59-64, 115-120, 128-133, 133-138, 257-262, 297-302

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FIGURE 154

MLVHCVGLLLTGLLGLTLGAGALLASEPIYQPPSAWVPAGGLVGLALLGALLTLRWPRPFTV
LGTTLGSAVLVACVDYFLEGLALGSWLGQRLQTLPALPSLC

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 38-55, 60-78

N-myristoylation sites.

amino acids 7-13, 12-18, 16-22, 22-28, 41-47, 50-56, 84-90, 88-94

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 67-78

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FIGURE 155

TGCAATTAAAGGAGTCGGGTCTCTAACTGTTGATCTGTTTTTTTCCCTTCTGAGCAATGGAGC
TTACCATCCTTTATCCTGAGACTGGCCATTTACATCCTGACATTTCCCTTGTACCTGCTGAAC
TTCTGGGCTTGTGGAGCTGGATATGCAAAAAATGGTTCCCCTACTTCTTGGTGAGGTTCACTG
TGATATACAACGAACAGATGGCAAGCAAGAAGCGGGAGCTCTTCAGTAACCTGCAGGAGTTTG
CGGGCCCTCCGGGAAACTCTCCCTGCTGGAAGTGGGCTGTGGCACGGGGGCCAACTTCAAGT
TCTACCCACCTGGGTGCAGGCTGACCTGTATTGACCCCAACCCCACTTTGAGAAGTTTTTGA
TCAAGAGCATTGCAGAGAACCGACACCTGCAGTTTGAGCGCTTTGTGGTAGCTGCCGGGGAGA
ACATGCACCAAGGTGGCTGATGGCTCTGTGGATGTGGTGGTCTGCACCCCTGGTGCTGTGCTCTG
TGAAGAACCAGGAGCGGATTCTCCGCGAGGTGTGCAGAGTGCTGAGACCGGGAGGGGCTTTCT
ATTTTCATGGAGCATGTGGCAGCTGAGTGTTTCGACTTGGAATTACTTCTGGCAACAAGTCCTGG
ATCCTGCCTGGCACCTTCTGTTTGATGGGTGCAACCTGACCAGAGAGAGCTGGAAGGCCCTGG
AGCGGGCCAGCTTCTTAAGCTGAAGCTGCAGCACATCCAGGCCCACTGTCTCTGGGAGTTGG
TGCGCCCTCATATCTATGGATATGCTGTGAAATTAGTGTGAGCTGGCAGTTAAGAGCTGAATGG
CTCAAAGAATTTAAAGCTTCAGTPTTACATTTAAATGCTAAGTGGGAGAAGAGAAACCTTTT
TTTTGGGGGGCGGTTTTTTTTGGTTTGTGTTGGTTTTTTTTTTTTTTTTTTTTTGGCAGGAGAATCTC
TTGAACCCAGAAGGCGAAGGTTGCAGTGAACCGAGATCATGCCATTGTACTCTAGCCTGGGTG
ACAAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAGTAGAGACAGGGAGAC
GGGGTCTCACTGTGTTGCCTAGGCCGCTCTTGAACCTCTGGGCTCAAGTGATTCTCCACCTT
GACCTCTTAAATGTTGGGATTACAGGTGTGAGACAGTGACCTGGCCGAAATAGCTCAAGTT
TCTGAAAAACAAATCTGAATCTATTGTTATTCTTAGCGTCACTGGTCTGGCTTTCAGAATTA
ACATACAAGGTTGCCACACCTAGTTCTGCCAGCTTTATGTCTTTTATCCAGTATTCCACCA
AAGTTTGTTTTCTGCATTCCAGTTCTCAAGTCTTAAGATAAAGATTGTACTTGACAGTTTAG
TATATCCATAAACTATTTGAGGTGGTTAAGGTTCTTGGGTTTCATTTTCTTAACTTTTGCT
GAATATTTGTAGATTGTAGGCAATGAAAAAGTCTACTAAATTAGGAAAACCTTGAATAATTAGG
TATCCTAGGTAAGAGCCCCATAACATCAAGCAATCTGTGAGTCTGTAAAGAAATAAATATTTT
TTGGATTATTCTTATCTAATTCACCCCTGTTGGAAGATGATTTCTTTGTTCTTTGCAACTAT
GGAAGCTGTGAAATCATCACAAGTGCCCTCTGAAAGCGAGTGTTAGGTTGGTTAGAGGGTTTA
ATATTTTCTGCAATGGTTTGTAGGAATTTTAATAAATGTAGTATATTTTCTGAGATGATTTTG
TAAAAGTACTATTTTAAATATCAAATCAACCAATAAATTCACATTTGTGTTAGGAACAAAA

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FIGURE 156

MELTIFILRLAIYILTFPLYLLNFGGLWSWICKKWFYFLVRFTVIYNEQMASKKRELFSLQ
EFAGPSGKLSLLEVGCSTGANFKFYPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAA
GENMHQVADGSVDVVCTLVLCVKNQERILREVCRLRPGGAFYFMEHVAAECSTWNYFWQQ
VLDPAWHLLFDGCNLTRESWKALERASFSLKLQHIQAPLSWELVRPHIYGYAVK

Signal peptide:

amino acids 1-29

N-glycosylation site.

amino acids 203-207

N-myristoylation sites.

amino acids 78-84, 80-86, 91-97, 201-207

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FIGURE 157

CCGCTGAGATGTACGAACTTCCGGTTCTCCGGGCAGCTGCCACTGCTGTAGCTTCTGCCACCT
GCCACGACCGGGCCCTCTCCCTGGCGTTTGGTCACCTCTGCTTCATTCTCCACCGCGCCTATGG
TCCCTCTTGGAGCCAGCGTGGCGGGCCTGGCGGCTCCCGGTTGGTGAGAGAGCGGTCCGGGAA
CGATGAAAGGCCCTCGCAGTGCTGCTGCTGCTGCTCAGCCACCTCTTGGCTTCCGTCTCTCCTGCG
TGTGCTGCCTGAACCTAAGCGGGCCCTGGCAGTCTGCTGCAGGCAGCCGAGGCCGCGCCAG
GTCCTTGGGCCTCCTGACCCCTAGACCACGGACATTACCGCCGCTGCCACCGGGCCCTACCCCTG
CCCAGCAGCCGGGCCGTGGTCTGGCTGAAGCTGCGGGGCCGCGGGCTCCGAGGGAGGCAATG
GCAGCAACCCCTGTGGCCGGCCTTGAGACGGACGATCACGGAGGGAAGGCCGGGGAAGGCTCGG
TGGGTGGCGGCCTTGCTGTGAGCCCCAACCTGGCGACAAGCCCATGACCCAGCGGGCCCTGA
CCGTGTTGATGGTGGTGAGCGGCGCGGTGCTGGTGTACTTCGTGGTCAGGACGCTCAGGATGA
GAAGAAGAAACCGAAAAGACTAGGAGATATGGAGTTTGGACACTAACATAGAAAATATGGAAT
TGACACCTTTAGAACAGGATGATGAGGATGATGACAACACGTTGTTTGATGCCAATCATCCTC
GAAGATAAGAATGTGCCTTTTGATGAAAGAACCTTTATCTTTCTACAATGAAGAGTGGAATTC
TATGTTTAAGGAATAAGAAGCCACTATATCAATGTTGGGGGGGTATTTAAGTTACATATATTT
TAACAACCTTTAATTTGCTGTTGCAATAAATACCGTATCCTTTTATTATATCTTTATATGTAT
AGAAGTACTCTATTAATGGGCTCAGAGATGTTGGGGATAAAGTATACTGTAATAATTTATCTG
TTTGAAAATTACTATAAAACGGTGTTTTCTGGTCGGTTTTTGTTCCTGCTTACCATATGATT
GTAAATTGTTTTATGTATTAATCAGTTAATGCTAATTATTTTTGCTGATGTCATATGTTAAAG
AGCTATAAATTCCAACAACCACTGGTGTAATAAATAATTTAAATTTCTTTACTGAAAGG
TATTTCCATTTTTGTGGGGAAAAGAAGCCAAATTTATTACTTTGTGTTGGGGTTTTTAAAAAT
ATTAAGAAATGTCTAAGTTATTGTTTGCAAAACAATAAATATGATTTTAAATTCCTTAAAAA
AAAAA

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FIGURE 158

MKASQCCCCLSHLLASVLLLLLLPELSGPLAVLLQAEEAAPGLGPPDPRFRTLFPPLPGPTPA
QQPGRGLAEAAAGPRGSEGGNGSNFVAGLETDDHGGKAGEGSVGGGLAVSPNPGDKPMTQRALT
VLMVVS GAVLVYFVVVRTVRMRRNRKTRRYGVLD TN IENMELT PLEQDDEDDNTLFDANHPRR

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 124-140

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.amino acids 69-75, 78-84, 81-87, 97-103, 103-109, 106-112,
157-160

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FIGURE 159

GCTGCAGGCGGCGACGGCTACACCA**ATG**GGCCGGCTGCTGCGGGCGCCCGGCTGCCGCCGCTG
CTTTCCGCGCTGCTGCTTCTGCTGGTTGGGGGAGCGTTCCCTGGGTGCCTGTGTGCCTGGGTCT
GATGAGCCTGGGCCAGAGGGCCTCACCTCCACCTCCCTGCTAGACCTCCTGCTGCCCACTGGC
TTGGAGCCTGGACTCGAGGAGCCTAGTGAGACCATGGGCCTGGGAGCTGGGCTGGGAGCC
TCTGGCTCAGGCTTCCCCAGCGAAGAGAATGAAGAGTCTCGGATTCTGCAGCCACCACAGTAC
TTCTGGGAAGAGGAGGAAGAGCTGAATGACTCAAGTCTGGACCTGGGACCCACTGCAGATTAT
GTTTTTCCCTGACTTACTGAGAAGGCAGGTTCCATTGAAGACACTAGCCAGGCTCAAGAGCTG
CCAAACCTCCCTCTCCCTTGCCCAAGATGAATCTGGTTGAGCCTCCCTGGCATATGCCTCCC
AGAGAGGAGGAAGAAGAGGAAGAGGAAGAGGAGGAGAGGGAGAAGGAAGAGGTAGAGAAACAA
GAGGAGGAGGAAGAGGAGGAGCTGCTCCCTGTGAATGGATCCCAAGAAGAAGCCAAGCCTCAG
GTCCGTGACTTTTCTCTCACCAGCAGCAGCCAGACCCAGGGGCCACCAAAGCAGGCGATGAA
GACTCCGGGGACCAGGCCTCATCAGGTGTGGAGGTGGAGAGCAGCATGGGGCCAGCTTGCTG
CTGCCTTCAGTCACCCCACTACAGTGACTCCGGGGGACCAGGACTCCACCAGCCAAGAGGCA
GAGGCCACAGTGCTGCCAGCTGCAGGGCTTGGGGTAGAGTTTCGAGGCTCCTCAGGAAGCAAGC
GAGGAAGCCACTGCAGGAGCAGCTGGTTTGTCTGGCCAGCACGAGGAGGTGCCGGCCTTGCCCT
TCATTCCTCAAACCACAGCTCCAGTGGGGCCGAGCACCCAGATGAAGATCCCTTGCTCT
AGAACCTCAGCCTCTTCCCCACTGGCCCTGGAGACATGGAACCTGACACCTTCTCTGCTACC
TTGGGACAAGAAGATCTCAACCAGCAGCTCCTAGAAGGGCAGGCAGCTGAAGCTCAATCCAGG
ATACCTCTGGGATTCTACGCAGGTGATCTGCAAGGACTGGAGCAATCTGGCTGGGAAAACTAC
ATCATTCTGAACATGACAGAGAACATAGACTGTGAGGTGTTCCGGCAGCACCGGGGGCCACAG
CTCCTGGCCCTGGTGGGAAGAGGTGCTGCCCCGCCATGGCAGTGGCCACCATGGGGCCTGGCAC
ATCTCTCTGAGCAAGCCCAGCGAGAAGGAGCAGCACCTTCTCATGACACTGGTGGCGGAGCAG
GGGTGGTGCCCACTCAAGATGTCTTTCCATGCTGGGTGACATCCGCAGGAGCCTGGAGGAG
ATTGGCATCCAGAACATTCCACAACCAGCAGCTGCCAGGCGGGGCCAGCCAGGTGCGCAGC
GACTACGGCACGCTCTTCGTGGTGTGGTGGTCATTGGGGCCATCTGCATCATCATATTGCG
CTTGGCTGCTCTACAACTGCTGGCAGCGCCGGCTGCCCAAGCTCAAGCACGTGTGCGACGGC
GAGGAGCTGCGCTTCGTGGAGAACGGCTGCCACGACAACCCACGCTGGACGTGGCCAGCGAC
AGCCAGTCGGAGATGCAGGAGAAGCACCCAGCCTGAACGGCGGGGGGCCCTCAACGGCCCCG
GGGAGCTGGGGGCGCTCATGGGGGGCAAGCGGGACCCGAGGACTCGGACGTGTTTCGAGGAG
GACACGCACCT**CTGA**CGCGAGCCGAGGCGCAGGCCAGTGGGGCCGACGACCAAGCGAGGTG
GACCCGAAACGGACGGCCGAGCCGACACCGCCCGCCCTACCCGGGCCGCCCGCCCGCG
CCTGGCCCTCGCGCGGGCTTCCTTCCCGCTTCCCCGACTTCACACGGCGGCTTCGGACCAAC
TCCCTCACTCCCGCCGAGGGGCGAGGCTCAAAGCCCGCCTTGCGCCCGCTTTCGCCCCCTG
AACCCGGCCCGCGGGCGCGGGCGCGCTTCCTGCGCCCGGAGTCAATTAACCCGCC
GGAGACCACGCCGGGCCAGCAAA

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FIGURE 160

MGRLLRAARLPPLLSPLLLLLLVGGAF LGACVAGSDEPGPEGLTSTSLDLLLPTGLEPLDSEE
PSETMGLGAGLGASGSGFPSEENEESRILQPPQYFWEEEEELNDSSLDLGPTADYVFPDLTEK
AGSIEDTSQAQELPNLPSPLPKMNLVEPPWHMFPREEEEEEEEEEREKEEVEKQEEEEEEEL
LPVNGSQEEAKPQVRDFSLTSSSQTPGATKSRHEDSGDQASSGVEVESSMGPSLLLPSTPTT
VTPGDQDSTSQEAETVLPAAGLGVEFEAPQEASEEATAGAAGLSGQHEEVPALPSFPQTTP
SGAEHPDEDPLGSRTSASSPLAPGDMELTPSSATLGQEDLNQQLLEGQAEEAQSRIPWDSTQV
ICKDWSNLAGKNYIILNM TENIDCEVFRQHRGPQLLALVEEVLPRHSGHHGAWHISLSKPSE
KEQHLLMTLVGEQGQVVPTQDVL SMLGDIRRSLEEIGIQNYSTTSSCQARASQVRS DYGTLFVV
LVVIGAICIIIIALGLLYNCWQRRLPKLKHVSHGEELRFVENGCHONPTLDVASDSQSEMQEK
HPSLNGGALNGPGSWGALMGKRPEDSDVFEEEDTHL

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 499-521

N-glycosylation sites.

amino acids 106-110, 193-197, 395-399, 480-484

Glycosaminoglycan attachment site.

amino acids 77-81

N-myristoylation sites.amino acids 24-30, 28-34, 41-47, 69-75, 71-77, 73-79, 75-81,
216-222, 327-333, 455-461, 519-525, 574-580, 581-587, 584-590**Amidation site.**

amino acids 588-592

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FIGURE 161

CCAGGGCGGAGCGCAGCTGCGCCGGGCTTGGGCGCCTGGGGCGCGCCTCCCCACCGTCGTTT
TCCCCACCGAGGCCGAGGCGCTCCCGGAGTCAATGGCCGGCCTGAACTGCGGGGTTCTCTATCGCA
CTGCTAGGGGTTCTGCTGCTGGGTGCGGCGCGCCTGCCGCGCGGGGCGAGAAGCTTTTGAGATT
GCTCTGCCACGAGAAAGCAACATTACAGTTCTCATAAAGCTGGGGACCCGACTCTGCTGGCA
AAACCCCTGTTACATCGTCATTCTTAAAGACATATAACCATGTTGTCCATCAAGTCTGGAGAA
AGAATAGTCTTTACCTTTAGCTGCCAGAGTCCTGAGAATCACTTTGTCTAGAGATCCAGAAA
AATATTGACTGTATGTCAGGCCCATGTCCTTTTGGGGAGGTTTCAGCTTCAGCCCTCGACATCG
TTGTTGCCCTACCTCAACAGAACTTTCATCTGGGATGTCAAAGCTCATAAGAGCATCGGTTTA
GAGCTGCAGTTTTCATCCCTCGCCTGAGGCAGATCGGTCCGGGTGAGAGCTGCCAGACGGA
GTCACTCACTCCATCAGCGGCCGAATCGATGCCACCGTGGTCAGGATCGGAACCTTCTGCAGC
AATGGCACTGTGTCCCGGATCAAGATGCAAGAAGGAGTGAAAATGGCCTTACACCTCCCATGG
TTCCACCCAGAAATGTCTCCGGCTTCAGCATTGCAAACCGCTCATCTATAAAACGTCTGTGC
ATCATCGAGTCTGTGTTTGAGGGTGAAGGCTCAGCAACCCGTGATGTCTGCCAACTACCCAGAA
GGCTTCCCTGAGGATGAGCTCATGACGTGGCAGTTTGTCTGTTCCGTGCACACCTGCGGGCCAGC
GTCTCCTTCCTCAACTTCAACCTCTCCAAGTGTGAGAGGAAGGAGGAGCGGGTTGAATACTAC
ATCCCGGGCTCCACCACCAACCCCGAGGTGTTCAAGCTGGAGGACAAGCAGCCTGGGAACATG
GCGGGGAAGTTCACCTCTCTCTGCAAGGCTGTGACCAAGATGCCCAAAGTCCAGGGATCCTC
CGGCTGCAGTTCCAAGTTTTTGGTCCAACATCCACAAAATGAAAGCAGTGAGTGAGAGCCCCACTT
TCCTTTTCTTCTCTCTCCAGCACCTTCGTTGTTTCTGGGTAGTCTGCCTGGGTGAGGCTCC
CTTCTGTTTCTCATCTGTGGCTTCTGAAACACTTAGACTCTGGACCCAGCAAGAGTTTCAGG
AAGTGGGTGTCTAGGCACTTAGACAGGCTTGTGGTGAACACCCGGTATGTAGTTCCATTTC
GCACAATAAAAAAGAAATCTTGCATTCAAGATGCTAAATTGTTTTTAACGAAAA

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FIGURE 162

MAGLNCGVSIALLGVLLLGAARLPRGAFAFEIALPRESNITVLIKLGTPTLAKPCYIVISKR
HITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGSPCFGEVQLQPSTSLPTLNRTFI
WDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSNGTVSRIKMQ
EGVKMALHLFPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANYPEGFPEDELMTW
QFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDKQPCNMAGNFNLSLQG
CDQDAQSPGILRLQFQVLVQHPQNESSE

Signal peptide:

amino acids 1-29

N-glycosylation sites.amino acids 39-43, 122-126, 180-184, 205-209, 213-217, 270-274,
310-314, 339-343**Tyrosine kinase phosphorylation site.**

amino acids 276-284

N-myristoylation sites.

amino acids 3-9, 7-13, 158-164, 175-181, 191-197, 303-309

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FIGURE 163

CAACCACACACCTGGGGAATTGCTGGCCTGACTTCTGACCCTGACTCCTCATACCTTCTCTC
CAGAGCATGACATTTGACCACCAACTGAAACCTGACCTCTGACCCAGACCACTGGCCCTTCC
CCCGCCCTGTGGTGACTTCATAAAGGTTACTAGCTTCTCCCTGGCCTTGAGACCCACACGAT
GGCCCTGCTGGCTCTGGCCAGTGCCGTCCTCTGCCCTGCTGGCCCTGGCTGTCTTCAGGGT
GCCCCCTGGGCTGTCTCTCTGCTTCACAACCTACTCTGAGCGCCTCCGCATCTGCCAGAT
GTTTGTGGGATGCGGAGCCCCAAGCTTGAAGAGTGTGAGGAGGCCTTCACGGCCGCTTCCA
GGCCCTCTCTGACACCGAAATCAGTGAGGAGACCATCCACACTTCATCAGTGTCTGGGGAAG
GTGCAGAGGGAGGGCAGGAGAGGGCCAGAGGGTCAGGCTGAGGGACAGACAGAGAGAACAGT
CAGAGGAGAAAGGCTCAAAGACCATGAGAACAACAGAGACTTAGGGACAGAGAGACACAGACA
GGGGAAGACAGCAGGGCAAGACTCAGAGAGGGGAGGATGGAGACTCAGAGAGGGGAAGATGG
AGACTCAGAGAGAGGGGAGGATGGAGACTCAGAGAGAGAGGAAGATGGAGACTCAGAGGGAAA
GATGGAGACTCAGGATATGGAGAGTCTCAGAGAGGGGAGGATGGAGACTCAGGGGAGGATGGAG
AGTCAGAGAGGATGGAGACTCATAGAAAAGGGGAGGATGGAGAGTCAAGGAGAGGTTGGAGACTGG
AGAGGGAATAGAGACCAGAAAAGGGGAGGATGGAGACTCAGAGGGTGGAAGATGGAGACTCAA
AGAGGATGGAAACCCAGAGAGAGGAGGACAGAGATGAGGCAGAGACTAGGGGAAGCAGGATAG
CGACTGGTCGGGGGCAGAGACTCAGGGAGGATAGAGACTCAGAGAGAGGTGAGGATAGAGACT
TGGGAGGGACTCAGGAAGCATAGCGACTGTGGGGCAAGAGTCTCAGAGAGGGGAGGATACAGAC
TTGGGAGGGCAGAGACTCAGAAACAGAATGTTGCGATTAGGGACATGGTGTTCGGGGAGCTG
CCTCCCCAGCCCCCTGCTCCCTCCCTCACCGCCAGACTATGATGAGAGAAGCCACCTGCATGA
CACCTTACCCAGATGACCATGCCCTGCAGGAGCTGGCTGCTGCCAGGGATCCTTTGAGGT
TGCTTCCCTGATGCTGCAGAGAAAATGAAGAAGGTCATTACACAGCTTAAAGAAGCCAGGC
TTGCATCCCTCCCTGCGGTCTCCAGGAGTTCGCCCCGGCGTTTCTCTGCAGCGGGTCTACTC
TAGGGTCTGCGACCTCCCGCTGGACTGCCAGTTCAGGATGTGACAGTGACTCGGGGCGACCA
GGCTATGTTTTCTTGATCGTAAACTTCCAGCTGCCAAAGGAGGAGATCACCTATTCTGGAA
GTTGCGCAGGAGGAGGTCTCCGGACTCAGGACTTGTCTATTTCAGAGATATGCCGCGGGCCGA
AGGATACCTGGCGGGATCCGGCCGGCTCAGCTCACGCACCGCGGGACGTTCTCTGCGTGAT
CAAGCAAGACCAGCGCCCCCTGGCCCGGCTCTACTTCTTTCTTAACGTCCTCGGGGCCCTCGC
ATCAGCGAGTGCGACAGTGTTGGCGTGTTGAGTTCTGGGGACTCCGGAGCCCCAGCATCTAGC
TCCCCGCTGTCTCAGATCCACCGAGAAGTCTGGGTTCAGCAACCTCCAACCCAGGAGGAT
GTTCTTTTCGATGGTACTGCAGTGGCACTAACAAAGGTATCTTTCTCTCTCCCTATCTTATT
TCCATCTGAAAATAAAGAATATATTTCAACTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 164

MALLALASAVPSALLALAVFRVPAWACLLCFTTYSERLRICQMFVGMRSFKLEECEEAFTAAF
QGLSDTEISEETIHTSSVSWGRRCRGRAGEAQRVRLRDRQRETVRGERLKDHENNRDLGTERHR
QGKTAGQRLREGRMESQRGEDGDSERGEDGDSEREEDGDSEKMETQEYGESEGGWTLRGGW
RVRRMETHRKGRMESQERLETGEGIETQKGEDGDSEGGRWRLKEDGNPERGGQR

Signal peptide:

amino acids 1-26

N-myristoylation site.

amino acids 65-71

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FIGURE 165

[illegible]

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FIGURE 166

MELSDVTLIEGVGNEVMVVGAVVVLILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGH
VDHLVAGQGNPEPTELPHPSEGNDKAEAEAGEGRGDSTGEAGAGGGVEPSLEHLLDIQGLPKR
QAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLNDTEELAVARPEDTVGALKSKYFFGQES
QMGLIYQGRLLQDPARTLRSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVGS
LMVPVFVVLGCVVYFRINRQFFFTAPATVSLVGVTVFFSFLVFGMYGR

Signal peptide:

amino acids 1-36

Transmembrane domains:

amino acids 246-267, 275-301

N-glycosylation sites.

amino acids 162-166, 211-215

N-myristoylation sites.

amino acids 48-54, 105-111, 109-115, 129-135, 177-183, 247-253

Cell attachment sequence.

amino acids 97-100

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FIGURE 167

GGCGGCTGTGTGTCGCCGGAGCCGAAGCGCGAGGCCGCTCCCGGTGGCCGGGGAGCGGGCGGGTGGGGGCGCC~~A~~
TGTGGTTCATGTACCTGCTGAGCTGGCTGTCGCTCTTCATCCAGGTGGCCTTCATCAGCGTGGCTGTCCGGGGCTG
GACTCTATTACTCGGCAGACTGTATGAGAAATACAGATGGCCACCAGCAGGATCATAAATACATGTATCTGGT
TCTCCACCGCTGTACTGTATTGGCCTCTACGCTCTTTGAGCGCTCCCCACCAGCATGATTGGAGTGGGCCATTCA
CCAACCTCGTCTACTTTGGCCCTCCCTCCAGACCTTCCCTTCATCATGCTGACCTCGCCTAACTTCATCTCTGCT
GTGGATAGTGGTGGTGAATCATTAACCTAGCATTTTCAGTTTTTGGCAGAAGAATATTATCCCTTCTCAGAGGTCC
TGCCCTATTTCACTTTCTGCCCTGTGGATAATTCGGTTTGGCGTTTTTGTGTCACTTTCGGCCGGGGAGAACGTCC
TGCCCTCTACCATGCAGCCAGGAGATGATGTCGTCTCCAATTATTTACCAAAGGCAAGCGGGGCAACGCTTAG
GGATCCTGGTTGTCTTCTCCTTCATCAAAGAGGCCATTCTACCCAGTCTGCAGAGAATATAC**TGA**CCCCATGCA
GGCAGGATGTGGGGGCAAGATCAGAGAGTCAAGGCCCTGGGCCCTCTATGCCAGGTGGGGACCAGAACTCGGGA
AGGCACCTACCACTGCCCTGGCTTCTTCCCCCAACTCTGGAGCCCCATCCCCACCTCCTTGGGGGGCTCAG
CTTGGCTCAGATCTGATGCTTCAAGAGGCTGTAACTCAGAGGGCACCAAGGAGGGTGGCAGAGCTGCTTAGCC
AGGAGGCGGAGGTCCCTCAGTCTCCCTGTCCCTTCCAAGGTGGGTGAGGAGGTTCTGGCCCGCTGGGGCGAGG
CAGGCGAGGCTCTGTGAAGCTTAAGACGAGATGGTGACAAGTCTCTGGCCAGGTGGCCATGGGAGGGGCCATG
GCTTGGCATGTCCAAGCAGAAATAGTTTTTGTGTTGAACGGTGATTTCTGTCCAAGTCAGAGTTTCCGTTTGAAT
AAAGCTTCGCTTCTAGGTGGCACTGTTTGCCTTAATACCTGCAGAGTTCATCTTCTTCTTCTCTCTGCTAAGCTTC
TGCTCTGACTGGACTCACTTTCTGTCTCAGGGACTCCTTTCTGSGTTTGGGCTCTGCCCTTCCCAAGGGACT
GTCTTTGTGGCCCTTAATGGGAAGGGGGCAGGGGTGAGGAGCTGAGCCTGCTCAAGGAGTGGGAAGTGGGGCTAT
AGGCAGCTCTCTGATGCATCTCTTCCACTCTTTTCCCAAGGCTCCGTGACTGTCAAACTGGGAGTAGGAGAG
GGGCAATTTAGGACTGGGCTAGATTTTCAGAAGAACATCTACAATATCCTATTTATAAATCTTCTCTGGGAAA
AGGAGTGGTTTTCTGGCTGAATATCTTAGGCTCAAGGAGAAACAAAATAAAATTAGCTTCCAGGACGCTGT
TTTTAAAGAAATGGGACTAATGGGAGAGCTGTTGTCACTCAAGAGCATCCAAGCCCTGGCCCGCTGTGTGCAC
CTTGGCTCTGGGGAGATATATCTGCCTTCAAGAAGGCGAGGCCAGGTCTTGGGCACAGACCTGCATTGTTGA
CCTTGCACTCCAACATATAGTGCCTTGAAGTGCTCAAGCAGTACATATTTGAATGAAGTCCCTATAGAGAGCATT
CTGGCCATGTTCTATACCTCAAAGTGAGGCTSGCAGTACAGAGATGAACCTACACATGTGATACATTTAAAGCC
ACTGCAAAAACCCCTGTGCTTGAAAAATTTTCTCTATATCATGCTGGAGTTCCATCATAGCCCTTCATTTCCT
TGGCTTTAGCATTTACCTTCTCTTAAGAATACAGCTTTCCTCTTCCCTGAGAGGAAGAGACATGTTGGTCTC
CTCTTAGTGTGAACGAGATTGCCAGGCCCTTTTCTCTATGCACACCAGGATAGACAAAGGCGAGGGATCTGGCA
GCCTGCATCATCTCCCATTTGGGCTGCAGCTGGCCCTACTTTCCTCCCTCTGCTGCTTGGTCCCTCAGCTTGTAT
GATGTGGCTTCGCCCTCCACTCTACTGCCAGTGTTCTCCAGGGGTTGCTAAATCCAGCAGACCCCTTTCCTG
TCTTACTAGATCTGGGCAGCACTTTGACATGGCTGATCACCCTTGTCTTCTGATGAGCACTTCCCTGGCAGCTCT
GTGGCTAGTTGTCTACCTCCCTGGCTGTCTTTCAGGCTTCGCTGCAGGCTTCTCCACTTGGCCATGCACAT
AGGGTCTTTCAAGGTTCTGCTGTGGGCTCCCTAGGGAAGCCCATCCATCTPGATGGTTCAAGGATGGTGAGGAA
TTTAGAGTTGACCTCCAGCCCAACATCCTTCTGATCACTGAACCAAGTTTTGCTGGCCCTTAGGTGCACAG
ACAATTCAGGTCATGGCCAGATGGTACTTGTGTCTTCTGCAAACTTGCCTTCTGGGATCTTCCCTTGACC
CCGAGATCACTCAGGAGCCAGCAGCAAGAACTTATGCTATTCCGTGTTTTCTCTTCTGCCACCACTCCAATCTC
TCAAAACGGTCAGGTCACTTACCATCTCTTGATTGAGCAGTCCCTGCTGTCATAGCTTTCACCTGGATTAT
CGTGACAGCCCTCACTGCTCTCTATCATGTGGCCAGAGATCTTCTCTAAATAGCATTCGATGTGATGAT
TCATCTCTGGCCATAAAGCTTCTTGGCTCCCTGCTGCCCTAGGATAAGTCTCGAACCCCTCAGCATGGCTTG
TGAGACTCATGGTGCTTGTCCCTGTCACTCTCTGCTCATCACTTGGCTCTGTGACTTCTGGGTCCAGC
CTCTGATCAGAGATGCAGTGGCTCTCATTGGCATCTGATTCCTTCTTTTGGTACAGAGAAAGGT
ACTTTCTCTGCAAACTCTCACTTAGACTTGACTTCTCCCAAGGAGCTTGGCTATACCTCTCTCTCCGACCCC
CACCTCTGGCATACACAGATCACTACAGCTTGGCTGCTTAATGGTCACTCTCCAGTCACTGTAAGC
TCTTGAAGGGCAAGGATTGTGTGAATTTTGTATTAACAGTGCCTGGCTTGGTGCCTGACACCTAGAAAGCAG
TCAATAAATGTTGTTTAATGA

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FIGURE 168

MWFMYLLSWLSLFIQVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIGLYVFE
RFPTSMIGVGLEFNLVYFGLLQTFPFIMLTSPNFILSCGLVVVNHYLAFQFFAEYYPFSEVL
AYTFFCLWIIIPFAFFVSLSAGENVLPSTMQPGDDVVSNYFTKGRGKRLGILVVFSFIKEAIL
PSRQKIY

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 126-146

Casein kinase II phosphorylation site.

amino acids 145-148

N-myristoylation sites.

amino acids 73-78, 82-87

Amidation sites.

amino acids 168-171, 171-174

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 91-101

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FIGURE 169

CAAAGCCCTACCCTCACCATTACCAGGTCCTGTGGGAAGAGCAGCGTGGAGGTGGGCTGAGG
TTAGAAGGTGCAGAGCGTGGGAAGAAGATTGTGAGCTGAGTATTGGACATCTGTTCTTGAATAG
TCCCTGGGCCTGCCATAGGAAAGGAAGTTCTCCAGGGTTACAGTTCTTATCCGCGTGAATACA
CATGGCTCTGTACGAAAAATTAATCAGGTGCTGCTGTTCTTCTGATCGTGACCCCTCTGTGT
GATTCTGTATAAGAAAGTTTATAAGGGGACTGTGCCAAGAATGACGCAGATGATGAATCCGA
GACTCCTGAAGAACTGGAAGAAGAGATTCTCTGGTGATTGTGTGCTGCAGCAGGGAGGATGGG
TGCCACTATGGCTGCCATCAATAGCATCTACAGCAACACTGACGCCAACATCTTGTTCTATGT
AGTGGGACTCCGGAATACTCTGACTCGAATACGAAAATGGATTGAACATTCCAAACTGAGAGA
AATAAACTTTAAATTCGTGGAATTCACCCGATGGTCCTCAAAGGGAAGATCAGACCAGACTC
ATCGAGGCCTGAATTGCTCCAGCCTCTGAACCTTTGTTGATTTTATCTCCCTCTACTTATCCA
CCAAACACGAGAAAGTCATCTATTGGACGATGATGTAATTGTACAAGGTGATATCCAAGAACT
GTATGACACCACCTTTGGCCCTGGGCCACGCGGGGCTTTCTCAGATGACTGCGATTTGCCCCTC
TGCTCAGGACATAAACAGACTCGTGGGACTTCAGAACACATATATGGGCTATCTGGACTACCG
GAAGAAGGCCATCAAGGACCTTGGCATCAGCCCAGCACCTGCTCTTTCAATCCTGGTGTGAT
TGTTGCCAACATGACAGAATGGAAGCACCAGCGCATCACCAGCAATTGGAGAAATGGATGCA
AAAGAATGTGGAGGAAAACCTCTATAGCAGCTCCCTGGGAGGAGGGGTGGCCACCTCCCCAAT
GCTGATTGTGTTTCATGGGAAATATTCCACAATTAACCCCTGTGGCACATAAGGCACCTGGG
CTGGAATCCAGATGCCAGATATTTCGGAGCATTTTCTGCAGGAAGCTAAATTACTCCACTGGAA
TGGAAGACATAAACCTTGGGACTTCCCTAGTGTTTACAACGACTTATGGGAAAGCTGGTTTGT
TCCTGACCCCTGCAGGGATATTTAAACTCAATCACCATAGCTTGATATAACTCTACCCTTAAAT
ATTCCCTGTATAGAAATGTGGAATTGTCCCTTTGTAGCCAACTATAACATTGTTCTTTATGAA
TATTACCTTTGATACATATGATCCACAATATAAAAAACCAAAACTACTGTGTGCAAAATTATAC
CTTGGACCATATAGGCATTGATTAACCTCTTTAAGTACATGTGATAACTATGGAATCAAGAT
TATGTGACTGAAAAACATAAAGGAAGAGACCATCTAGATAACAGCAATCAACCTGCTTAATT
CTGAATGACAATTATATCCACAATTTTTTAAACTTCTACATGTATTTTCACATGAAGATCT
CCTTAACAGGTTGCCAACCTTTTCTTTTATAAACTATTACATTTAAAAATATGGACGCTCGAA
AAATAAAATATTCATCATTTTTTAAAA

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FIGURE 170

MALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESETPEEEEEEIPVVICAAAGRMG
ATMAAINSIYSNTDANILFYVVGRLNTLTRIRKWIEHSKLRRETNFKIVEFNPMVLKGGKIRPDS
SRPELLQPLNFVRFYLPLLIHQHEKVIYLDLDDVIVQGDIQELYDTTLALGHAAAFSDDCDLPS
AQDINRLVGLQNTYMGYLDYRKKAIKDLGISPSTCSFNPGVIVANMTEWKHQRIITKQLEKWMQ
KNVEENLYSSSLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFLQEAKLLHWN
GRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 234-238

Tyrosine kinase phosphorylation site.

amino acids 253-261

N-myristoylation sites.amino acids 63-69, 86-92, 198-204, 218-224, 229-235, 265-271,
266-272

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FIGURE 171

GCCAGAGGCTGCAGCTGGAGCCCAGAGCCCAAGATGGAGCCCCAGCTGGGGCCTGAGGCTGCC
GCCCTCCGCCCTGGCTGGCTGGCCCTGCTGCTGTGGGTCTCAGCCCTGAGCTGTTCTTTCTCC
TTGCCAGCTTCTTCCCTTTCTTCTGCTGGTGCCCCAAGTCAGAACCAGCTACAATTTTGAAGG
ACTTTCCTCGGTCTTGATAAATGCAATGCCTGCATCGGGACATCTATTGCAAGAAGTCTTT
AAAGAAGAAATAAGATCTGACAACCTGGCTGGCTTCCACCTTGGACTGCCTCCCGATTCCCTTG
CTTTCTTATCCTGCAAATTACTCAGATGATTCCAAAATCTGGCGCCCTGTGGAGATCTTTAGA
CTGGTCAGCAAATATCAAAACGAGATCTCAGACAGGAGAATCTGTGCCTCTGCATCAGCCCCA
AAGACCTGCAGCATTGAGCGTGTCTGCGGAAAACAGAGAGGTTCCAGAAATGGCTGCAGGCC
AAGCGCTCACGCCGACCTGGTGCAGGACTGTCACCAGGGCCAGAGAGAACTAAAGTTCCTG
TGTATGCTGAGATTAACACCAGTGAAAAAGCCTGGCATGGAGCCCAGCACTGAGAACCTCCAGA
AAGTGTTAGCCTTCTCCCAACTGTGTTATACCAACCACATTTTCAAATAGTAATCATTAAGA
GGCTTCTGCATCAAA

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FIGURE 172

MEPQLGPEAAALRPGWLALLLWVSALSCSFSLPASSLSSLVPQVRTSYNFGRTFLGLDKCNAC
IGTSICKKFFKEEIRSDNWLASHLGLPPDSLLSYPANYSDDSKIWRPVEIFRLVSKYQNEISD
RRICASASAPKTCSEIERVLRKTERFQKWLQAKRLTPDLVQDCHQGQRELKFLCMLR

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 100-103

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 158-161

N-myristoylation sites.

amino acids 56-61, 65-70

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 18-28

Prenyl group binding site (CAAX box).

amino acids 179-182

Leucine zipper pattern.

amino acids 5-26

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FIGURE 173

GCTGGACTGCTCGCTGGCCGGCAGCGCACCGTTTTGAAGGTCCTAGCCCACCTGGGCTGGCTC
ACGCGCACGACTAGCCGCTCCCATACAGCACGCCCGGACTCTGTCTCGCTTAAGGCCACTCC
TATTCTACGGGTGACCCCTGGTGGTCACGTGGATCTGTTCCGCCACGCAAGTCTGGGTCCCTCG
GCGATTGACCGGGTCTTGTCTGTTCTGGGAGCCTCTCCTAAGCTGCCTGTTCTGCGCGAGAGTT
TGGAGGGCGGGTTTGGGGTCGGTGTCTGATTGGGGCTCGCACCGCAGCACGCTGGAGTCCCG
CTTAGGTACCAAGTTAGCGTCAGGGGAGCTGGGTTCAGGCGGTCTGCCGGGACACCCCGTGTGG
CAGGCGGCGAAGCGCTCTGGAGAATCCCGGACAGCCCTGCTCCCTGCAGCCAGGTGTAGTTTC
GGGAGCCACTGGGGCCAAAGTGAGAGTCCAGCGGTCTTCCAGCGCTTGGGCCACGGCGGCGGC
CCTGGGAGCAGAGGTGGAGCGACCCATTACGCTAAAGATGAAAGGCTGGGGTTGGCTGGCCC
TGCTTCTGGGGCCCTGCTGGGAACCGCTGGGCTCGGAGGAGCCAGGATCTCCACTGTGGAG
CATGCAGGGCTCTGGTGGATGAACTAGAAATGGGAAATTGCCAGGTGGACCCCAAGAAGACCA
TTCAGATGGGATCTTTCCGGATCAATCCAGATGGCAGCCAGTCAAGTGGGAGGTGCCTTATG
CCCGCTCAGAGGCCACCTCACAGAGCTGCTGGAGGAGATATGTACCGGATGAAGGAGTATG
GGGAACAGATTGATCCTTCCACCCATCGCAAGAACTACGTACGTGTAGTGGGCCGGAATGGAG
AATCCAGTGAACTGGACCTACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCTCAAGT
TTGCGTGTGAGAGCATTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGG
CTGACAATGTTAAAGACAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACA
TATCGCATGATGAGCTATGAACCCTGGAGCAGCCCACTGGCTTGATGGATACCCCCAGG
AGGGGAAAATGGTGGCAATGCCTTTTATATATTATGTTTTTACTGAAATTAAGTAAAAATA
TGAAACCAAAGT

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FIGURE 174

MKGWGWLALLLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSFRINPDGS
QSVVEVPYARSEAHLTELEEICDRMKEYGEQIDPSTHRKNYVRVVGRRNGESSELDLQGIRID
SDISGTLKFACESIVEEYEDELIEFFSREADNVKDKLCSKRTDLCDHALHISHDEL

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 12-18, 16-22, 29-35

Endoplasmic reticulum targeting sequence.

amino acids 179-184

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FIGURE 175

CGCAGCGCGGCAGTCTCTGATGCGCCCGGCATGGGTTACCGCTGCTGCCCTGCTGTGCGTCTCTG
GTCGGCGCGTGGCTCAAGCTAGGAAATGGACAGGCTACTAGCATGGTCCAACGTCAGGGTGGG
AGATTCCTGATGGGAACAAATTCTCCAGACAGCAGAGATGGTGAAGGGCCTGTGCGGGAGGCG
ACAGTGAACACCTTTGCCATCGACATATTTCTGTGACCAACAAGATTTCAGGGATTTTGTCT
AGGGAGAAAAAGTATCGGACAGAAGCTGAGATGTTTGGATGGAGCTTTGTCTTTGAGGACTTT
GTCTCTGATGAGCTGAGAAACAAAGCCACCCAGCCAATGAAGTCTGTACTCTGGTGGCTTCCA
GTGGAAAAGGCATTTTGGAGGCAGCCTGCAGGTCTCTGGCTCTGGCATCCGAGAGAGACTGGAG
CACCCAGTGTATTACACGTGAGCTGGAATGACGCCCGTGCCTACTGTGCTTGGCGGGGAAAACGA
CTGCCCACGGAGGAAGAGTGGGAGTTTGCCGCCCGAGGGGGCTTGAAGGTCAGTTTACCCA
TGGGGGAAGTGGTTCCAGCCAAACCGCACCAACCTGTGGCAGGGAAGTTCCCCAAGGGAGAC
AAAGCTGAGGATGGCTTCCATGGAGTCTCCCCAGTGAATGCTTTCCCGCCCAGAACAACCTAC
GGGCTCTATGACCTCCTGGGGAACGTGTGGGAGTGGACAGCATCACCGTACCAGGCTGCTGAG
CAGGACATGCGCGTCTCTCGGGGGGCATCCTGGATCGACACAGCTGATGGCTCTGCCAATCAC
CGGGCCCCGGGTCAACCACAGGATGGGCAACACTCCAGATTGAGCCTCAGACAACCTCGGTTTC
CGCTGTGCTGCAGACGCAGGCCCGGCCCGAGGGGAGCTGTAAAGCAGCCGGGTGGTGACAAGGA
GAAAAGCCTTCTAGGGTCACTGTCAATCCCTGGCCATGTTGCAACAGCGCAATTCCAAGCTC
GAGAGCTTCAGCCTCAGGAAAGAACTTCCCCTTCCCTGTCTCCCATCCCTCTGTGGCAGGCGC
CTCTCACAGGGCAGGAGAGGACTCAGCCTCCTGTGTTTTGGAGAAGGGGCCAATGTGTGTT
GACGATGGCTGGGGGCCAGGTGTTTCTGTTAGAGGCCAAGTATTATTGACACAGGATTGCAAA
CACACAAACAGTTGGAACAGAGCACTCTGAAAGGCCATTTTTTAAGCATTTTAAATCTATTTC
TCTCCCCCTTTCTCCCTGGATGATTCAGGAAGCTGACATTGTTTCTCAAGGCAGAATTTTCC
TGGTCTGTGTTTTCTCAGCCAGTTGCTGTGGAAGGAGAATGCTTTCTTTGTGGCCTCATCTGTG
GTTTCGTGTCCCTCTGAAGGAACTAGTTTCCACTGTGTAACAGGCAGACATGTAACATTTTA
AAGCACAGTTCACTCCTAAAGGGTCTGGGAGAACAGATGATGTACTAGTGAAGCATTGCA
TTGTGGGAATCAGAAAGCAAATAGTACTCCAGAAAGACAAATATCAGAAGCTTCCTATTCTTT
TTTTTTTTTTTTTTTTTTTTTTTGTAGACAGGGTCTTTCTCTGTTGCCAGGCTAGAGTGCAGT
GTGATCAGCGCTCACTCTAGCCTTGAATTCTTGGGCCCAAGCAATTCTCCCACCTCAGCCTCC
TGAGTAGCTGGGACTACAAGTGTGACCAACCATGCCTGGCTAATTTTTTGAATTTTGTAGTG
ATGGGATCTCGCTCTGTTGCCAGGGTGGTCTCGAACTCCTGGCCTCAAGCGATCCTCCACC
TCGACCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACCTCGCCTGGGCCCTTCTCCATA
TGCTCCAAAAACATGTCCCTGGAGAGTAGCCTGCTCCCACTGTCTACTGGATGTATGGGG
CCATAAAATCTCCTGCAATTGTGTATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

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FIGURE 176

MARHGLPLLPLLSLLVGAWLKLGNQATSMVQLQGGRFLMGNTNSPDSRDGEGPVREATVKPFA
IDIFPVTNKDFRDFVREKKYRTEAEMFGWSFVFEDEVSDIELRNKATQPMKSVLWWLPVEKAFFW
RQPAGPGSGIRERLEHPVLHVSWNDARAYCAWRGKRLPTEEEWEFAARGGLKGQVYPWGNWFQ
PNRTNLWQGKFPKGDKAEDGFHGVSPVNAFFPAQNNYGLYDLLGNVWEWTASPYQAAEQDMRVL
RGASWIDTADGSANHRARVTTTRMGNTFDSASDNLGFRCAADAGRPPGEL

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 191-195

N-myristoylation sites.

amino acids 23-29, 25-31, 175-181

Amidation site.

amino acids 159-163

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FIGURE 177

GCCTTCTCGCGCCTGACCATGCACCCCTGCATCTTCTGCTGGGCCACAGGCGAGCGCTTTAT
TTCTGGAGCTGAGGGCTAAAACCTTTTTTGACTTTTCTTCTCCTCAACATCTGAATCATGCCAT
GTGCCCAGAGGAGCTGGCTTGCAAACCTTTCCGTGGTGGCTCAGCTCCTTAACCTTTGGGGCGC
TTTGCTATGGGAGACAGCCTCAGCCAGGCCCGGTTTCGCTTCCCGACAGGAGGCAAGAGCATT
TTATCAAGGGCCTGCCAGAATACCACGTGGTGGGTCCAGTCCGAGTAGATGCCAGTGGGCATT
TTTTGTGCTATGGCTTGCACTATCCCATCACGAGCAGCAGGAGGAAGAGAGATTGGATGGCT
CAGAGGACTGGGTGTACTACAGAATTTCTCACGAGGAGAAGGACCTGTTTTTAACCTTGACGG
TCAATCAAGGATTTCTTTCCAATAGCTACATCATGGAGAAGAGATATGGGAACCTCTCCCATG
TTAAGATGATGGCTTCTCTGCCCCCTCTGCCATCTCAGTGGCACGGTCTACAGCAGGGCA
CCAGAGTTGGGACGGCAGCCCTCAGTGCCTGCCATGGACTGACTGGATTTTTCCAACCTACCAC
ATGGAGACTTTTTCATTGAACCCGTGAAGAAGCATCCACTGGTTGAGGGAGGGTACCACCCGC
ACATCGTTTACAGGAGGCAGAAAGTTCCAGAAACCAAGGAGCCAACCTGTGGATTAAAGGGTA
TTGTGACTCACATGTCTCTGGGTGAAGAATCTGTTTTGTTCTTTTGGTTAGTTTTATTAAA
ACATGACCTATTCTTACTCAAGTCTCTTATCTCCTCTGTATTCTTTTTTTTTTAATATCTTCA
TGACATTCAAATCTCTTCTGTATTCTCTGCCAGAAAGTGACATTCTTTTTTGCTTGATAAAA
CCCTTTCACCTTGTC